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Sequence Listing was accepted.

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Reviewer: Durreshwar Anjum

Timestamp: [year=2007; month=12; day=2; hr=14; min=49; sec=27; ms=527;]

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Application No: 10558627

Version No: 2.0

Input Set:

Output Set:

Started: 2007-11-14 09:19:11.293

Finished: 2007-11-14 09:19:12.820

Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 527 ms

Total Warnings: 18

Total Errors: 0

No. of SeqIDs Defined: 21

Actual SeqID Count: 21

Error code	Error Description
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W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
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<110> Eli Lilly and Company

<120> GLP-1 Analog Fusion Proteins

<130> X-15984

<140> 10558627

<141> 2005-11-29

<150> 60/477880

<151> 2003-06-12

<160> 21

<170> PatentIn version 3.3

<210> 1

<211> 31

<212> PRT

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<220>

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<222> (2)..(2)

<223> Xaa at position 2 is Gly or Val

<400> 1

His	Xaa	Glu	Gly	Thr	Phe	Thr	Ser	Asp	Val	Ser	Ser	Tyr	Leu	Glu	Glu
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Gln	Ala	Ala	Lys	Glu	Phe	Ile	Ala	Trp	Leu	Val	Lys	Gly	Gly	Gly
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<223> Xaa at position 2 is Gly or Val

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His Xaa Glu Gly Thr Phe Thr Ser Asp Val Ser Ser Tyr Leu Glu Glu
1 5 10 15

Gln Ala Ala Lys Glu Phe Ile Ala Trp Leu Lys Asn Gly Gly Gly
20 25 30

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His Xaa Glu Gly Thr Phe Thr Ser Asp Val Ser Ser Tyr Leu Glu Glu
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Gln Ala Ala Lys Glu Phe Ile Ala Trp Leu Val Lys Gly Gly Pro
20 25 30

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His Xaa Glu Gly Thr Phe Thr Ser Asp Val Ser Ser Tyr Leu Glu Glu
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Gln Ala Ala Lys Glu Phe Ile Ala Trp Leu Lys Asn Gly Gly Pro
20 25 30

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Gln Ala Ala Lys Glu Phe Ile Ala Trp Leu Val Lys Gly Gly
20 25 30

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Gln Ala Ala Lys Glu Phe Ile Ala Trp Leu Lys Asn Gly Gly
20 25 30

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 <223> Xaa at position 17 is Phe, Val, or Ala

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Ala Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Xaa
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Xaa Xaa Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
 20 25 30

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
 35 40 45

Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly
 50 55 60

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Xaa
 65 70 75 80

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
 85 90 95

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro
 100 105 110

Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
 115 120 125

Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn
130 135 140

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
145 150 155 160

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
165 170 175

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg
180 185 190

Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys
195 200 205

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
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Ser Leu Ser Leu Gly Xaa
225 230

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Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
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<210> 9
<211> 31
<212> PRT
<213> Homo sapiens

<400> 9

His Ala Glu Gly Thr Phe Thr Ser Asp Val Ser Ser Tyr Leu Glu Gly
1 5 10 15

Gln Ala Ala Lys Glu Phe Ile Ala Trp Leu Val Lys Gly Arg Gly
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<220>
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<400> 10

His Gly Glu Gly Thr Phe Thr Ser Asp Val Ser Ser Tyr Leu Glu Glu
1 5 10 15

Gln Ala Ala Lys Glu Phe Ile Ala Trp Leu Val Lys Gly Arg Gly Gly
20 25 30

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
35 40 45

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Glu Ser
50 55 60

Lys Tyr Gly Pro Pro Cys Pro
65 70

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<220>
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<400> 11

Trp Leu Val Lys Gly Arg Gly Gly Gly
1 5

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<400> 12

Trp Leu Val Lys Gly Gly Gly

1 5

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<400> 13

Trp Leu Lys Asn Gly Gly Gly
1 5

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Trp Leu Val Lys Gly Gly Pro
1 5

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<400> 15

Trp Leu Lys Asn Gly Gly Pro
1 5

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<400> 16

Trp Leu Val Lys Gly Gly
1 5

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Trp Leu Lys Asn Gly Gly
 1 5

<210> 18
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 <400> 18

Pro Pro Cys Pro Ser Cys
 1 5

<210> 19
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<400> 19

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 1 5 10 15

Ser Gly Gly Gly Gly Ser
 20

<210> 20
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 tctggtggcg gtggcagcgc tgagtccaaa tatggtcccc catgcccacc ctgcccagca 180

cctgaggccg cggggggacc atcagtcttc ctgttcccc caaaacccaa ggacactctc 240
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 gaggtccagt tcaactggta cgtggatggc gtggaggtgc ataatgcca gacaaagccg 360
 cgggaggagc agttcaacag cacgtaccgt gtggtcagcg tcctcacctg cctgcaccag 420
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 atcgagaaaa ccatctccaa agccaaaggg cagccccgag agccacaggt gtacacctg 540
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 ttctaccca ggcacatcgc cgtggagtgg gaaagcaatg ggcagccgga gaacaactac 660
 aagaccagc ctcccgctgct ggactccgac ggctccttct tcctctacag caggctaacc 720
 gtggacaaga gcaggtggca ggaggggaat gtcttctcat gctccgtgat gcatgagget 780
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<400> 21

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 1 5 10 15

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 20 25 30